

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Polymeropoulos, Michael
Lavedan, Christian
Leroy, Elisabeth
Nussbaum, Robert
Johnson, William
Duvoisin, Roger

(ii) TITLE OF INVENTION: Cloning of a gene mutation for
Parkinson's disease

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 25-JUN-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Schneller, John W.
(B) REGISTRATION NUMBER: 26,031
(C) REFERENCE/DOCKET NUMBER: NIH 0082A

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: alpha synuclein gene/ exon 4 region

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4
(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTAATCAGC AATTAAAGGC TAGCTTGAGA CTTATGTCTT GAATTTGTTT TTGTAGGCTC	60
CAAAACCAAG GAGGGAGTGG TGCATGGTGT GACAACAGGT AAGCTCCATT GTGCTTATAT	120
CAAAGATGAT ATNTAAAGTAT CTAGTGATTA GTGTGGCCA GTATCAAGAT TCCTATGAA	181
ATTGTAAAACA ATCACTGAGC ATCTAAGAAC ATATC	216

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTAATCAGC AATTAGGCT AG	22
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer #13"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTATACAAGA ATCTACGAGT C

21

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37840

(vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Val	Phe	Met	Lys	Gly	Leu	Ser	Lys	Ala	Lys	Glu	Gly	Val	Val
1															15

Ala	Ala	Ala	Glu	Lys	Thr	Lys	Gln	Gly	Val	Ala	Glu	Ala	Ala	Gly	Lys
															30
									20						25

Thr	Lys	Glu	Gly	Val	Leu	Tyr	Val	Gly	Ser	Thr	Lys	Glu	Gly	Val	
									35						40

Val	His	Gly	Val	Ala	Thr	Val	Ala	Glu	Lys	Thr	Lys	Glu	Gln	Val	Thr
															50
															55

Asn	Val	Gly	Gly	Ala	Val	Val	Thr	Gly	Val	Thr	Ala	Val	Ala	Gln	Lys
															65
															70

Thr	Val	Glu	Gly	Ala	Gly	Ser	Ile	Ala	Ala	Ala	Thr	Gly	Phe	Val	Lys
															85

Lys	Asp	Gln	Leu	Gly	Lys	Asn	Glu	Glu	Gly	Ala	Pro	Gln	Glu	Gly	Ile
															100
															105

Leu	Glu	Asp	Met	Pro	Val	Asp	Pro	Asp	Asn	Glu	Ala	Tyr	Glu	Met	Pro
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115

120

125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37377

(vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
 1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
 20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
 35 40 45

Val His Gly Val Thr Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
 50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
 65 70 75 80

Thr Val Glu Gly Ala Gly Asn Ile Ala Ala Ala Thr Gly Phe Val Lys
 85 90 95

Lys Asp Gln Met Gly Lys Gly Glu Glu Gly Tyr Pro Gln Glu Gly Ile
 100 105 110

Leu Glu Asp Met Pro Val Asp Pro Ser Ser Glu Ala Tyr Glu Met Pro
 115 120 125

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala

130

135

140

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bos taurus*
(C) INDIVIDUAL ISOLATE: Swiss-Prot P33567

(vii) IMMEDIATE SOURCE:

(B) CLONE: alpha synuclein protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Phe	Met	Lys	Gly	Leu	Ser	Met	Ala	Lys	Glu	Gly	Val	Val
1				5					10					15	

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
 20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
 35 40 45

Val	Gln	Gly	Val	Ala	Ser	Val	Ala	Glu	Lys	Thr	Lys	Glu	Gln	Ala	Ser
50						55						60			

His	Leu	Gly	Gly	Ala	Val	Phe	Ser	Gly	Ala	Gly	Asn	Ile	Ala	Ala	Ala
65						70					75				80

Glu Pro Glu Gly Glu Ser Tyr Glu Glu Gln Pro Gln Glu Glu Tyr Gln
 115 120 125

Glu Tyr Glu Pro Glu Ala
130

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Serinus canaria
 - (C) INDIVIDUAL ISOLATE: genbank L33860
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: alpha synuclein homologue

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Torpedo californica*
- (C) INDIVIDUAL ISOLATE: Swiss-Prot P37379

(vii) IMMEDIATE SOURCE:

- (B) CLONE: alpha synuclein homologue

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Val Leu Lys Lys Gly Phe Ser Phe Ala Lys Glu Gly Val Val
1 5 10 15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Gln Asp Ala Ala Glu Lys
20 25 30

Thr Lys Gln Gly Val Gln Asp Ala Ala Glu Lys Thr Lys Glu Gly Val
35 40 45

Met Tyr Val Gly Thr Lys Thr Lys Glu Gly Val Val Gln Ser Val Asn
50 55 60

Thr Val Thr Glu Lys Thr Lys Glu Gln Ala Asn Val Val Gly Ala
65 70 75 80

Val Val Ala Gly Val Asn Thr Val Ala Ser Lys Thr Val Glu Gly Val
85 90 95

Glu Asn Val Ala Ala Ala Ser Gly Val Val Lys Leu Asp Glu His Gly
100 105 110

Arg Glu Ile Pro Ala Glu Gln Val Ala Glu Gly Lys Gln Thr Thr Gln
115 120 125

Glu Pro Leu Val Glu Ala Thr Glu Ala Thr Glu Glu Thr Gly Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #1F"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGACAGTGT GTGTAAAGG

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #13R"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACATCTGTC AGCAGATCTC

20

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 2809 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 139A20 HUMAN BETA SYNULEIN GENE

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGCCGCAGC CGCCGCTCCA TCCCCAGCCC CGGCCCGCA TCCGGTTGG AAGGGGGCTG
CAAGTTGCA AGGGGCCGG GANAAAANC GAGCAGTGGC CCTTCCCGCG TCCCCAGGGT
TTCAAGGGAC GCTAGGANTN TCCGCGGCC TGGAGGTTCG CACTGGGAG TGGGGTGAGA
TGGGGGAAA GCAGGGAGGG GCTCAGGGTC CAGAAGGGCN CCGCGGTCTC GGGAGTAGGG
GGGCATNTGC GTCCCGCGGG AGGGGCTGGG GTGAGAGTGC GGGGCCAGTG CACCGGTGCC
CGTGTATCGC CCTCCCCAGG CCGCCAGGAT GGACGTGTTC ATGAAGGGCC TGTCCATGGC
CAAGGAGGGC GTTGTGGCAG CCGCGGAGAA AACCAAGCAG GGGGTACCG AGGCGGCCGA
GAAGACCAAG GAGGGCGTCC TCTACGTCGG TGGCNGGGG GCNGGGTTTC TGGGGCTGCA
GGGCTGGGG TCCCCCTACA GTGTGGAGCT GGGGCCGGT CCCGGGGAGG GGGGTTCTGG
GCAAGATAAT ATNANTCAGC AGATGGGCN AGTCANCAN GGGTCATAAG GGACATAACCC
ANCCCATAGA ANCCTGGTC TGTATCCGGA AATGGGGACA CGGGGCGGGC TGATGAGGTG
GGGGGCTCCA NCTGAAAGGC CAGGGACCAN TGCANTNATA AAANCACACA NCCTCCTTTT
TCTTATCTTT TTTACCATTA TTAATAGTTA TCTGGTGGT AACTCTTCT GTATGCCAAG
TACTGGTAA AATGTCATAA CATCCATTTC CTCATGTAAT GCTTCCGCC ATTCTACAGG
TAAGGGAAAC TGGGCTTCCC ATTGGTAGNT AAATTTAGG TTCAGAAAGG CTTGAATTGA
ATGTCAGTTC AGCCAATTTC TTAGTGGTGG AACCAAAC TG AGTTCCATCC GTGAAACGGG
GACAATAACA GCACCCGCTT CCCAGGGCTG GGGAAAAGTG AAGTGCAGCG GGGCAGGCAG
AGGACTTGAC ACAGCACTGG CCCTCAGCCA ACATCCACTA GAGGGTGGG GTATGCATC
AGGTGGAGA GAACTGCAAC CCTTGCAGAC AGAGGTGTGG GGCCCAGTGC AGTGATAAGA
CGGGGTTAA CATGGGGGTG CAGGTTGTAG GATNTGGGA CCCAAGGAGG CAGTGACGGG
GCCAGGATGC CCACTCTGTA ATCACCAGTC TGTGCTGGAG TTTCTGTTCC CTCAGCGCAG
AGTCCTTAAA TGTGCCGCTT TTTCTNCCCT GCAGGAAGCA AGACCCGAGA AGGTGTGGTA
CAAGGTGTGG CTTCAGGTAC TAGCCCAGCC CTGGCACCAAG CCCTCTCTC AMTTAGGCGG
ATGATCTGGC CGGGAACCAAG AGGGCGGGGG CGGGGGAGAC TCCCAAGGCT TCTGCGGGAA
TGCTCCGTGG GGAGGGCAGG CCCTGGGATA CTACAAGGCA GGGCATCGGT GTTCCCCCT
GGCTCCAAA CCCCTTCCTC AACCCCCCTCC CTGCTCCAGT GGCTGAAAAA ACCAAGGAAC

AGGCCTOACA TCTGGGAGGA GCTGTGTTCT CTGGGGCAGG GAACATCGCA GCAGCCACAG
 GACTGGTGAA GAGGGAGGAA TTCCCTACTG ATCTGAAGGT AAGCGATCCT TCTGACCCGC
 ACATGCAGGC AAACACACAC ACACACACAC ACACACACCN GGCACACAAA TAAACCTGTC
 ACCATCCCCG CCCCCCTAAT CCTGCCACCA GCTTGGAAACA CAAGCCACTT TGCCTCCCAT
 CCTGCNGGCC CGTGCTAGAC TCAGCTCAGA ATGCATCTGA ATAANGCGT GCATGGGTGT
 GACGCTCCCG GTGATGGGA CCCAGACCTG GCTGTCTGCG TGTATCCTGC TTGCCAGCGT
 GACCCATATG ACTTCTGGCC ACGTCTGCAT GTGTCAATGA TTGTTCATTC ATTTCTTTTC
 ATTCAACAAA TATCCATGCC ANANCCAGCC CTGTCCTTGA GCTTCCAGNT CCCTTCAGC
 CNAGGGGAGC NTGAGGGTTA TTTTTGGGT CCCGATGCC AGCACAGAGC CTGACACAAA
 GGATGAGGCA TAAGCTGGTG ANTGAGTATC CAAATGGTGG AAGTGTGGAG GNTGCCAGGC
 ATTGGGGGAG CGGCCTGGAG AGCCAGCTCC CCAATCCATG CTGCCACTTC AACTGTGATT
 CGGGGAATT TCCCCCTTCA CCTCCATCCC ACTTCCAAGG CACTCCAAAT AAATAACTGA
 ATTAGAAATT ATCCTTGT TT TGCCAACCCA CCCTAGCCTT CCCCCACTCCA ACCCACCCAA
 AGCTTACAC TGTGGGAATT TGGGGGCAT CCTGGCTGTC CTCACGAGTC CTGACCTTTT
 CTGCCACAG CCAGAGGAAG TGGCCCAGGA AGCTGCTGAA GAACCCTGA TTGAGCCCCT
 GATGGAGCCA GAAGGGGAGA GTTATGAGGA CCCACCCAG GAGGAATATC AGGAGTATGA
 GCCAGAGGCG TAGGGGCCCA GGAGAGCCCC CACCAGCAGC ACAATTCTGT CCCTGTCCCT
 GCCCCGCCAG CCAGAGCCAG GGCTGTCCTT AGACTCCTTC TCCCCAATCA CGAGATCTTC
 CTTCCGCTCT GAGGCAACCC CCTCGGAGCC TGTGTTAGTG TCTGTCCATC TGTCTGTCCT
 ACCCGCCCGC GTCCAACCCC GGGCATGGA CAGGGCCAGG GTTGCCTGCG CGGCTGGGAG
 CCTCGCCCT CCAGTGTGCTCCTCCCAT CCAGCGTCTG CGCG

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 223 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 5' END

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGGAGATCC AGCTCCGTCC TGCCTGCAGC AGCACAAACCC TGCACACCCA CCATGGATGT
CTTCAAGAAG GGCTTCTCCA TCGCCAAGGA GGGNGTGGTG GGTGCGGTGG AAAAGACCAA
GCAGGGGTG ACGGAAGCAG CTGAGAAGAC CAAGGAGGGG GTCATGTATG TGGGATTACA
TTTTTTTTT AAAGAAAGAA TAAATTAATT GTGATTAAAG TTG

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 677

(B) TYPE NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

(A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 3' END

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTNAGG GGGGAAAACA GGGATANAA AAANANGGGG GGGGGTTTTT NNNGGGGGGG
GGGGAAAANG GTTNGGGGN NAACCNAAN AAANNCCNAN GGGGGGGNN ANTNAANTTT
TGGGAACCCA AAGCCCNAGG AGGATTTTN GTNAANAACG TNACCTCNAG TGGGNCGAGG

AAGACCAAGG AAANGCCCAA CNCGGTTGAN CGAGGCTGTG GTGAACANCG TNAACNCTG
TGCCCNCCAA NANCGTGGAG GNGGCGGAGA ACATCSCGGT CACCTCCGGG GTGGTGCAG
AGGAGGACTT GAGGCCATCT KCCCCCCMAC AGGAGGGTGT GGCATCCMAA GARAAAGAGG
AAAGTGGCAGA GGAGGCCAG AGTGGGGAR ACTAGAGGGC TACAGGCCAG CGTGGATGAC
CTGAAGAGCG CTCCCTGTGCC TTGGACACCA TCCCCTCCTA GCACAAGGAG TGCCCGCCTT
GAGTGACATG CGGCTGCCA CGCTCCTGCC CTCGTCTTCC TGGCCACCC TGGCCTGTCC
ACCTGTGCTG CTGCACCAAC CTCACTGCC TCCCTCGGCC CCACCCACCC TCTGGTCCTT
CTGACCCAC TTATGCTGCT GTGAATTTTT TTTTTAAATG ATTCCAAATA AAACTTGAGC
CCACTCCAAA AAAAAAA

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1181 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exons 1 and 2 plus
flanking intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTCAGCG ATGGGAGGGC AAAGCGCTCT CGGCGGTGCG GTGTGAGCCA CCTCCCGGCG
 CTGCCTGTCT CCTCCAGCAG CTCCCCAAGG GATAGGCTCT GCCCTTGGTG GTCGACCCCTC
 AGGCCCTCGN TCTCCCAGGN CGACTCTGAC GAGGGGTAGG GGGTGGTCCC CNGGAGGACC
 CAGAGGAAAG GCNGGGACAA GAAGGGAGGG GAAGGGGAAA GAGGAAGAGG CATCATCCCT
 AGCCCAACCG CTCCCGATCT CCACAAGAGT GCTCGTGACC CTAAACTTAA CGTGAGGC
 AAAAGCGCCC CAACCTTTTC CGCCTTGNN CCAGGCAGGC GGCTGGAGTT GATGGCTCAC
 CCCCGGCCCG CTGCCCCATC CCCATCCGAG ATAGGGACGA GGAGCACGCT GCAGGGAAAG
 CAGCGAGCGC CGGGAGAGGG CGGGGCAGAA GCGCTGACAA ATCAGCGGTG GGGCGGAGA
 GCCGAGGAGA AGGAGAAGGA GGAGGACTAG GAGGAGGAGG ACGGCGACGA CCAGAAGGGG
 CCCAAGAGAG GGGCGAGCG ACCGAGCGCC GCGACCGAA GTGAGGTGCG TGCGGGCTCA
 GCGCAGACCC CGGCCCGGCC CCTCCTGAGA GCGTCCTGGG CGCTCCCTCA CGCCTTGCCT
 TCAAGCCTTC TGCCTTCCA CCCTCGTGA CGGAGAACTG GGAGTGGCCA TTCGACGACA
 GGTTAGCGGG TTTGCCTCCC ACTCCCCAG CCTCGCGTCG CCGGCTCACA GCGGCCTCCT
 CTGGGACAG TCCCCCCCAG GTGCCCTCCGCCCTCCTG TGCGCTCCTT TTCCCTCTTC
 TTTCTATTAA AATATTATTT GGGATTGTT TAAATTTTTT TTTTAAAAAA AGAGAGAGGC
 GNGGAGGAGT CGGAGTTGTG GAGAACGAGA GGGACTCAGG TAAGTACCTG TGGATCTAAA
 CGGGNGTCTT TTGGAAATCC TGGAGAACGC CGGATGGAGA CGAATGGTCG TGGGNACCGG
 GAGGGGGTGG TGCTGCCATG AGGACCGCTG GGCCAGGTCT CTGGGAGGTG AGTACTTGTC
 CTTTGGGAG CTAAGGAAAG AGACTTGACC TGGCTTCGT CCTGCTTCTG ATATTCCCTT
 CTCCACAAAGG GCTGAGAGNT TAGGCTGCTT CTCCGGGATC C

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 536 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 3 plus flanking
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTAAAAGAG TCTCACACTT TGGAGGGTTT CTCATGATTT TTCAGTGT TTTGTTTATT
TTTCCCCGAA AGTTCTCATT CAAAGTGTAT TTTATGTTT CCAGTGTGGT GTAAAGAAAT
TCATTAGCCA TGGATGTATT CATGAAAGGA CTTTCAAAGG CCAAGGAGGG AGTTGTGGCT
GCTGCTGAGA AAACCAAACA GGGTGTGGCA GAAGCAGCAG GAAAGACAAA AGAGGGTGT
CTCTATGTAG GTAGGTAAAC CCCAAATGTC AGTTGGTGC TTGTTCATGA GTGATGGT
AGGATAACAA TACTCTAAAT GCTGGTAGTT CTCTCTCTTG ATTCAATTGC GCATCATTGC
TTGTCAAAAAA GGTGGACTGA GTCAGAGGTA TGTGTAGGTA GGTGAATGTG AACGTGTGTA
TNTGAGCTAA TAGTAAAAAT GCGACTGTTT GCTTTTCAGA TTTTTAATT TGCTAATAT
NTATGACTTN TAAATGAA TGTTCTGTA CTACATAATT CTATNTCAGA GACAGT

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 650 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 4 plus flanking
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCAGGTCA ACGGATCTGT CTCTAGTGCT GTACTTTAA AGCTTCTACA GTTCTGAATT
CAAAATTATC TTCTCACTGG GCCCCGGTGT TATCTCATTTC TTTTTCTCC TCTGTAAGTT
GACATGTGAT GTGGGAACAA AGGGGATAAA GTCATTATTG TGTGCTAAAA TCGTAATTGG
AGAGGACCTC CTGTTAGCTG GGCTTCTTC TATNTATTGT GGTGGTTAGG AGTCCTTCT
TCTAGTTTA GGATATATAT ATATATTTT TCTTCCCTG AAGATATAAT AATATATATA
CTTCTGAAGA TTGAGATTTT TAAATTAGTT GTATTGAAAA CTAGCTAATC AGCAATTAA
GGCTAGCTG AGACTTATGT CTTGAATTG TTTTGAGG CTCCAAAACC AAGGAGGGAG
TGGTGCATGG TGTGGCAACA GGTAAGCTCC ATTGTGCTTA TATCAAAGAT GATATNTAAA
GTATCTAGTG ATTAGTGTGG CCCAGTATCA AGATTCTAT TGAAATTGTA AAACAATCAC
TGAGCATCTA AGAACATATC AGTCTTATTG AACTGAATT CTTTATAAAG TATTTTTAAA
TAGGTAATAA TTGATTATAA ATAAAAAATA TACTTGCCAA GAATAATGAG

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 504 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 5 plus flanking
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATATCTTAGC CAAGATTCAA TGTGTTGGTTG AACCACACTC ACTTGACATC TTGGTGGCTT
TTGTTCTTC TGACCACTCA GTTATCTATG GCATGTGTAG ATACAGGTGT ATGGAANCAGA
TGGCTAGTGG AAGTGGAATG ATTTTAAGTC ACTGTTATTC TACCACCCCTT TAATCTGTTG
TTGCTCTTTA TTTGTACCAAG TGGCTGAGAA GACCAAAGAG CAAAGTACAA ATGTTGGAGG
AGCAGTGGTG ACGGGTGTGA CAGCAGTAGC CCAGAAGACA GTGGAGGGAG CAGGGAGCAT
TGCAGCAGCC ACTGGCTTTG TCAAAAAGGA CCAGTTGGGC AAGGTATGGC TGTGTACGTT
TTGTGTTACA TTTATAAGCT GGTGAGATTA CGGTTCAATT TCATGTGAAG CCTGGAGGCA
GGAGCAAGAT ACTTACTGTG GGGAACGGCT ACCTGACCCCT CCCCTGTGA AAAAGTGCTA
CCTTTATATT GGTCTTGCTT GTTT

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 727 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exons 1 and 2 plus
flanking intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAAAGTTTAC ATACTTGAG GTTGATAACC CATGTTGCCG CAATGTTCC CCGGAGGCAT
TGTGGAGTTT AGAATGCCAG TAGTAATATT AAGGTGTGCC ATTTTCAAGA TCCGTGGCCA
ACATCCCTAT ATGTAAGATT TTTCCAAAAC ATGGTTCTGA TTTTAAAG TGAAAAATGC
TACTTCATCA TGTTCTTTT GTGCTTCTTA CTTTAAATAT TAGAATGAAG AAGGAGCCCC
ACAGGAAGGA ATTCTGGAAG ATATGCCTGT GGATCCTGAC AATGAGGCTT ATGAAATGCC
TTCTGAGGTA GGAGTCCAAG CTGAATCTTT CTAACAAGAC AGTACCAAAA ACCTGTCATT
GTCACATTTC TCTTCATTA GTGCTTAGTG AGAACATTG GCTCTCTACA TGCTCATTA
GTGGACAAGTGAA GAATAGTTT TACATTTTA AAGGGTCCTT AAAAAAAAAG
AGGAGGAGGA AGATGAAGAA GAGGAAGAAA GGATGTAAAA GAAATCATAT GTAGTCCACA
TAGCTTAATA TACNTACTAC TTGACCCCTT ACAGGAAAAG CTTTACTAAC CCCTGCATTA
GAGAATATAT TTTTTGCAA AAACATTGAT TGTAAATTG AGTGTAAAGT GGGGAGCCAT
TTCCTATCTC ATTGGCTGTC CAGTGCTGAT GCGTAATTGA AACTTATACT AACAGTGTGT
GCTGTCT

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1596 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 7 plus flanking
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTGATTTC TCTAATATTA GGAAGGGTAT CAAGACTACG AACCTGAAGC CTAAGAAATA
TCTTGCTCC CAGTTCTTG AGATCTGCTG ACAGATGTT ACATCCTGTAC AAGTGCTCAG
TTCCAATGTG CCCAGTCATG ACATTTCTCA AAGTTTTAC AGTGTATCTC GAAGTCTTCC
ATCAGCAGTG ATTGAAGCAT CTGTACCTGC CCCCCACTCAG CATTCCGGTG CTTCCCTTTC
ACTGAAGTGA ATACATGGTA GCAGGGCTT TGTGTGCTGT GGATTTGTG GCTTCAATCT
ACGATGTTAA AACAAATTAA AAACACCTAA GTGACTACCA CTTATTCTA AATCCTCACT
ATTTTTGTG TGCTGTTGTT CAGAAGTTGT TAGTGATTG CTATCATATA TTATNAGATT
TTTAGGTGTC TTTAATGAT ACTGTCTAAG AATAATGACG TATTGTGAAA TTTGTTAATA
TATATNATAC TTAAAAATAT GTGAGCATGA AACTATGCAC CTATAATACT AAATATGAAA
TTTACCAATT TTGCGATGTG TTTTATTCAAC TTGTGTTGT ATATNAATGG TGAGAATTAA
AATAAAACGT TATCTCATG CAAAAATATT TTATTTTAT CCCATCTCAC TTTAATAATA
AAAATCATGC TTATAAGCAA CATGAATTAA GAACTGACAC AAAGGACAAA AATATAAAGT
TATTAATAGC CATTGAGAAGA AGGAGGAATT TTAGAAGAGG TAGAGAAAAT GGAACATTAA
CCCTACACTC GGAATTCCCT GAAGCAACAC TGCCAGAAGT GTGTTTGTT ATGCACTGGT
TCCTTAAGTG GCTGTGATTA ATTATTGAAA GTGGGGTGT GAAGACCCCA ACTACTATTG

TAGAGTGGTC TATTCTCCC TTCAATCCTG TCAATGTTG CTTTACGTAT TTTGGGGAAC
TGTTGTTGA TGTGTATGTG TTTATAATTG TTATACATTG TTAATTGAGC CTTTTATTAA
CATATATTGT TATTTTGTC TCGAAATAAT TTTTAGTTA AAATCTATTT TGTCTGATAT
TGGTGTGAAT GCTGTACCTT TCTGACAATA AATAATATNC GACCATGAAT AAAAAAAA
AAAAAGTGGG TTCCCGGGAA CTAAGCAGTG TAGAAGATGA TTTTGAACAC ACCCTCCTTA
GAGAGCCATA AGACACATTA GCACATATTA GCACATTCAA GGCTCTGAGA GAATGTGGTT
AACTTTGTTT AACTCAGCAT TCCTCACTTT TTTTTTTAA TCATCAGAAA TTCTCTCT
CTCTCTCTTT TTCTCTCGCT CTCTTTTTT TTTTTTTTT TTTTACAGGA AATGCCTTTA
AACATCGTTG GGAACCTACCA GAGTCACCTT AAAGGGAGNA TCAATTCTCT AGGACTGGAT
AAAAATTCA TGGGCCTCCT TTAAAATGTT GCCCAAATAT ATGGAATTCT AGGGGTTTT
CCNTAGGGGG AAGGGTTTTT TCTCTTTCN GGGGAGGATC CTTTAACNC CCCNGGGGG
NGCCCGGAAA ATAAACTTGG NGGGGGGGNA AAACCTT